

METHOD AND SEQUENCES FOR DETERMINATE NUCLEIC ACID HYBRIDIZATION

ABSTRACT OF THE DISCLOSURE

5

Provided are methods for using nucleic acid sequences having two or more
degenerately pairing nucleotides, each degenerate nucleotide having a partially
overlapping set of complementarity, to reduce the number of hybridizing nucleotide
sequences or probes used in biochemical and molecular biological operations having
10 sequence specific hybridization. The method may be employed for various hybridization
procedures with sequence specific hybridization, including sequencing methods
measuring hybridization directly, and tagging by hybridization methods in which the
sequence is determined by analyzing the pattern of tags that hybridize thereto, and
hybridization dependent amplification methods. The method involves hybridizing to the
15 nucleic acid sequence of interest a first hybridizing nucleotide sequence and a second
hybridizing nucleotide sequence, each comprising a sequence complementary, or
complementary except at a position of interest or variable position, to a nucleic acid
sequence of interest, and analyzing the whether some, all or none of the probes or tags
hybridize.

20